

| | 10 | 20 | 30 | 40 | 50 | |
|---------|---|-----|-----|--------------|-----|-----|
| NOV_HU | MQSVQSTSFCRLRKQCLCLTFLLLHLLGQVAAT----- | | | | | 32 |
| CTGF_H | MTAASMGPVRAVFVLLALCSRPAVG----- | | | | | 26 |
| zctgf2M | ----- | | | | | 0 |
| zctgf4H | MQGLLFPTLLLAGLAQFCCRQG----- | | | TGPLDTTPEGRP | | 35 |
| IBP1_H | MSEVPVARVWLVLVLLLTQVGVTAG----- | | | | | 25 |
| IBP2_H | MLPRVGC PALPLPPPLLPLLPLLLLLLGASG-GGGGARAEVLFRCPPCT | | | | | 49 |
| | 60 | 70 | 80 | 90 | 100 | |
| NOV_HU | -----QRCPPQCPGRCPATP-PTCAPGVRAVL DGCSCCLVCARQR | | | | | 71 |
| CTGF_H | -----QNC\$GPCR--CPDEPAPRCPAGVSLVLDGC GCCRVC AKQL | | | | | 64 |
| zctgf2M | ----- | | | | | 0 |
| zctgf4H | GEVSDAPQRKQFCHWPCK-CPQQK-PRC PPGVSLVRDGC GCKI CAKQP | | | | | 82 |
| IBP1_H | ---APWQCAPCSAEKLAL--CPPVS-ASCSEVTR--SAGCGCCPMCALPL | | | | | 67 |
| IBP2_H | PERLAACGPPP VAPPAAVAAVAGGARMPCAELVR--EPGCGCCSVCARLE | | | | | 97 |
| | 110 | 120 | 130 | 140 | 150 | |
| NOV_HU | GESCS DLEPCDESSGLYCDRSADPSN-QTGICTAVEGD-NCVFDGVIYRS | | | | | 119 |
| CTGF_H | GELCTERDPCDPHKGLFCDFGSPANR-KIGVCTAKDGA-PCIFGGTVYRS | | | | | 112 |
| zctgf2M | ----- | | | | | 0 |
| zctgf4H | GEICNEADLCDPHKG LYCDYSVDRPRYETGV CAYLVAV-GCEFNQVHYHN | | | | | 131 |
| IBP1_H | GAACGVATARCARGLSCR----- | | | | | 85 |
| IBP2_H | GEACGVYTPRCGQGLRCY----- | | | | | 115 |
| | 160 | 170 | 180 | 190 | 200 | |
| NOV_HU | GEKFQPSCKFQCTCRDGQIGCVPRCQLDVLLEPNCPAPRKVEVPGE CCE | | | | | 169 |
| CTGF_H | GESFQSSCKYQCTCLDGAVGCMPLCSMDVRLPSPDCPFPRRVKLPGKCCE | | | | | 162 |
| zctgf2M | ----- | | | | | 0 |
| zctgf4H | GQVFQP NPLFSCLCVSGAIGCTPL--FIPKLAGSHCSGAK---GGKKSD | | | | | 175 |
| IBP1_H | ----- | | | | | 85 |
| IBP2_H | ----- | | | | | 115 |
| | 210 | 220 | 230 | 240 | 250 | |
| NOV_HU | KWICGPDEEDSLGGL---TAA YRPEATLGVEVSDSSVNCIEQTTEWTAC | | | | | 216 |
| CTGF_H | EWVC--DEPK-DQTVVGPALAAYRLED TFGPDPTMIRANCLVQTTEWSAC | | | | | 209 |
| zctgf2M | -----NVV YLPAYRN LPLIWKKKCLVQATK WTPC | | | | | 29 |
| zctgf4H | QSNC--SLEP---LLQQLSTS YK TMPAYRN LPLIWKKKCLVQATK WTPC | | | | | 219 |
| IBP1_H | ----- | | | | | 85 |
| IBP2_H | ----- | | | | | 115 |

Fig. 1A

| | 260 | 270 | 280 | 290 | 300 | |
|---------|---|------------|----------|-----|-----|-----|
| NOV_HU | SKSCGMGFSTRVTNRNRQCEMLKQTRLCMVRPCEQEPEQ- | PTDKKGKKCL | | | | 265 |
| CTGF_H | SKTCGMGISTRVTNDNASCRLEKQSRLCMVRPCEADLE-- | ENIKKGKKCI | | | | 257 |
| ZCTGF2M | S----- | | IPRGETCQ | | | 38 |
| zctgf4H | SRTCGMGISNRVTNENSNCMRKEKRLCYIQPCDSNILKTIKIPKGKTCQ | | | | | 269 |
| IBP1_H | ----- | | | | | 85 |
| IBP2_H | ----- | | | | | 115 |
| | 310 | 320 | 330 | 340 | 350 | |
| NOV_HU | RT-KKSLKAIHLQFKNCTSLLHTYKPRFCGVCS DGR C CTPHNTKTIQA EFQ | | | | | 314 |
| CTGF_H | RTPKISKPIKFE-LSGCTSMKTYRAKFCGVCTDGR C CTPHRTTLPVEFK | | | | | 306 |
| ZCTGF2M | PTFQLPKAEKFV-FSGCSSTQSYRPTFCGICLDKRCCVPNKS KMITVRFD | | | | | 87 |
| zctgf4H | PTFQLSKAEKFV-FSGCSSTQSYKPTFCGICLDKRCCIPNKS KMITIQFD | | | | | 318 |
| IBP1_H | ----- | | | | | 85 |
| IBP2_H | ----- | | | | | 115 |
| | 360 | 370 | 380 | 390 | | |
| NOV_HU | CSPGQIVKKPVMVIGTCTCHTNCPKNNEAFLQ ELELKTTRGK-- | | | | | 356 |
| CTGF_H | CPDGEVMKKNM MF IKTCACHYNCPGDNDIFESLYR KMYGDM-- | | | | | 348 |
| ZCTGF2M | CPSEGSFKWQMLWVTSCVCQRDCREP GDI FSEL RIL----- | | | | | 123 |
| zctgf4H | CPNEGSFKWKMLWITSCVCQRNCREP GDI FSEL KIL----- | | | | | 354 |
| IBP1_H | ----- | | | | | 85 |
| IBP2_H | ----- | | | | | 115 |

Fig. 1B